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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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February 17, 2006, 14:34:01; Search time 7245 Seconds (without alignments) 3601.262 Million cell updates/sec

Run on:

Title:

US-09-967-237B-2 2424 1 MAPLCPSPWLPLLIPAPAPG......RRGTKGGVSYRPAEVAETGA 459 Perfect score:

0.5 7.0 7.0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Scoring table: Seguence:

5883141 segs, 28421725653 residues Searched:

11766282 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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GenEmbl:* Jatabase

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description SUMMARIES a Query Match Length DB Score

Result

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Merkx,G., Figdor,C.G., Adema,G.J. and Oostervijk,E. Molecular cloning and immunogenicity of renal cell accinome-associated antigen G250 Int. J. Cancer 85 (6), 865-870 (2000) (bases 1 to 1519) Oosterwijk, E. PUBMED REFERENCE AUTHORS TITLE JOURNAL JOURNAL TITLE

Direct Submission Submitted (26-AUG-1998) Oosterwijk E., St. Radboud Academic Hospital Nijmegen, Urological Research Laboratory, Postbus 9101, 6500 HB Nijmegen, THE NETHERLANDS Location/Qualifiers

FEATURES

AJ010588 Homo sapi AR074439 Sequence AR081119 Sequence

HAJ10588 AR074439 AR081119

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Sequence 1 from patent US 5955075.
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1 (bases 1 to 1522)

RS Zavada,J., Pastorekova,S. and Pastorek,J.

Rethod of inhibiting tumor growth using ant

NAL Patent: US 5955075-A 1 21-SEP-1999;

Location/Qualifiers

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                             GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla
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GIGGAAGGCCACCGTTTCCCTGCCGACATCCACGTGGTTCACCTCAGGACCGCCTTTGCC
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(S Zavada,J., Pastorekova,S. and Pastorek,J.
MN proteins, polypeptides, fusion proteins and
AL Patent: US 5972353-A 1 26-OCT-1999;
Location/Qualifiers
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S Zavada,J., Pastorekova,S. and Pastorek,J.

MN-specific antibodies and hybridomas

MN-specific antibodies and hybridomas

I patent: US 5981711-A 1 09-NOV-1999;

Location/Qualifiers

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AR088064 Sequence 1 from patent | AR088064

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Zavada, J., Pastorekova, S. and Pastorek, J.
Zavada, J., Pastorekova, S. and Pastorek, J.
Immunological methods of detecting MN proteins and MN polypeptides
Patent: US 5989838-A 1 23-NOV-1999;
Location/Qualifiers
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1 MetAlaProLeuCysProSerProTrpLeuProLeuLeulleProAlaProAlaProGly 20		GAGGATCTACCTGGAGGATCTACCTGGAGGAGGATCTACCTGAAGTTAAGCCT 31 LysSerGludluGluGlySerLeuLySLeuGluAspLeuProThrValGluAlabroGly 12 ABATCAGAAGAGGCTCCCTGAAGTTAGAGGATCTACCTACTGTTGAGGCTCCTGGA 37 AspProGlnGluProGlnAsnAsnAshAsisArgAspLySGluGlyAspAspGlnSerHis 14	373 GATCCTCAAGAACCCCAGAATAATGCCCCACAGGGACAAAGAAGGGGGATGACCAGAGTCAT 43.2 141 TrpArgTyrG1ydapProProTrpProArgValSerProAlaCysAlaG1yArgPhe 160 151 [cccadcraccaccrrcraccagaccrr proproleuprogluteuargleuarga 	201 SerValGinLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220 	221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThr 240	261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280	853 GAGGGCCCGGAAGAAACAGTGCCTATGAGCGTTGCTCTCCGCTTGGAAGAATCGCT 912 301 GluGluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320 913 GAGGAAGAGCTTCAGAGATTCAGAGATTCAGAGATTCGAGCATTGAGCATCTGCCTTCTGCCTTCTGAC	PheserangTyrPheGluTyrGluGlySerLeuThrThrProProCysAlaGluGlyVal
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Qy 241 ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260 Db 733 GTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGGGTTCACCTCAGGACGCCTTTGCC 792 Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280 Db 793 AGAGTTGACGAGGCCTTGGGGGGCCCGGGAGGCCTGGTGGTGGCGCCTTTCTGGAG 852 Qy 281 GluGlyProGluGluAanSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300 Ch 1	Qy 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360 Db 1033 ATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGCGCTCCACACCCTCTCT 1092 Qy 361 AspThrLeuTrpGlyAProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380 Db 1093 GACACCCTGTGGGACCTCGGGCTACAGCTACAGCTACAGCGACGCACGC	Qy 381 LeuAshGlyArgVall1eGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400 Db 1153 TrGAATGGGCGAGTGATTGAGGCTCCTCCTCCTGCTGGAGTGGACAGCAGTCCTCGGGCT 1212 Qy 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420 AD 11 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420	421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlmetArgArgGlnHisArg 1273 GGCCTCCTTTTTGCTGTCACCGGGTTCCTTGTGCAGTGAGGCAGCAGAGA	Oy 441 ArgGlyThrLysGlyGlyOalSerTyrArgProAlaGluValAlaGluThrClyAla 459 	RESULT 6 AR104223 AR104223 LOCUS LOCUS DEFINITION Sequence 1 from patent US 6093548. ACCESSION AR104223 VERSION AR104223.1 GI:12816931 KEYWORDS SOURCE UNKNOWN.	Σ	Source 1. 1522 Source Source Source Source Source Source Source Source Source Source Source Sou	Alignment Scores: 6.2e-103 Length: 1522 Score: 2424.00 Matches: 459 Score: 100.0\$ Conservative: 0 Best Local Similarity: 100.0\$ Mismatches: 0 Query Match: 100.0\$ Indels: 0 DB: 6 Gaps: 0

121 AspproGinGlubroGinAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140	281 GluGlyProGluGluAenSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla [11] [11] [11] [11] [11] [11] [11] [11]	DD 1033 ATCTGGACTGTGTTTAACCAGACAGGACAGGACAGGACA
QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380 Db 1093 GACCCTCTCGGGGGACCTCGGGCTAACTTCCGGGGAGCCAGCTT 1152 QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400 Db 1153 TrGAATGGGCGAGTGATTGAGGCTCCTTCCCTGCTGAGTGGACACCTCTCTCGGGCT QY 401 AlaGluProValGluEuArgAGGCTCCTTCCTGCTGGTGACACCTCGTGGTGTGACACCTGGTTTTT QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMecArgArgGlnHisArg 440 Db 1273 GCTCCTTTTGCTGTCACCTGGCTGCTGGTGACATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	Advada, J., rastorekova, S. and rastorek, M. gene and protein Patent: US 6204370-A 1 20-MAR-2001; Location/Qualifiers 11522 / organism="unknown" / mol_type="unassigned DNA" / mol_type="unassigned DNA" Scores: 6.2e-103 Length: 2444.00 Matches: 100.0\$ Conservative: Similarity: 100.0\$ Mismatches: 6 Gaps:	US-09-967-237B-2 (1-459) x AR143487 (1-1522) Oy

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Zavada,J., Pastorekova,S. and Pastorek,J.
MN gene and protein
Patent: US 6297051-A 1 02-0CT-2001;
Location/Qualifiers
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                         M. Unknown.
Unclassified.
E 1 (bases 1 to 1522)
S Zavada, J., Pastorekova, S. and Pastorek, J.
MN gene and protein
AL Patent: US 6297041-A 1 02-OCT-2001;
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1522)
S Zavada,J., Pastorekova,S. and Pastorek,J.
MN gene and protein
L Patent: JP 2002528085-A 1 03-SEP-2002;
INSTITUTE OF VIROLOGY
OS Homo sapiens (human)
PN JP 2002528085-A/1
PD 03-SEP-2002
PF 22-OCT-1999 JP 2000578465
PR 23-OCT-1999 US 09/17776,23-OCT-1998 US 09/178115 PI
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NO SERVICE (Human)

PN JP 2002528085-A/1

PD 03-SEP-2002

PF 22-OCT-1999 US 09/17776,23-OCT-1998 US 09/178115 PI

JAN ZAVADA, SILVIA PASTOREKOVA, JAROMIR PASTOREK PC

CIZNIS/09, AGIK39/00, AGIK39/395, AGIK39/395, AGIK48/00, AGIP35/00, PC

COTRALS/09, AGIK39/02, GOIN33/566//(CI2Q1/02,CI2R1:91),CI2NI5/00,AGIK37/02

CC MN gene and protein

FH Key

Location/Qualifiers

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                                                               LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla
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BD243152.1 GI:33052922
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Zavada,J., Pastorekova,S. and Pastorek,J.

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Patent: US 6770438-A 1 03-AUG-2004;

Institute of Virology, Slovak Academy of Sciences; Bratislava;

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AR575998 Sequence 5 f AR575998 AR575998.1

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Zavada,J., Pastorekova,S. and Pastorek
NN gene and protein
Patent: US 6774117-A 5 10-AUG-2004;

Institute of Virology, Slovak Academy
CZX;
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/mol_type="genomic DN
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Hominidae; Homo.
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                                           Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G. Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using seene sets
Patent: WO 0194629-A 3116 13-DEC-2001;
Avalon Pharmaceuticals (US)
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Human; carbonic anhydrase; tumour; antigen; cytostatic; gene; ss.
                                                                                      Human carbonic anhydrase isozyme CA IX coding sequence
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ALIGNMENTS
                                                                                                                                       Location/Qualifiers
1. .1380
                                   ADL70155 standard; cDNA; 1380 BP
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SUMMARIES

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The present sequence is the coding sequence for human carbonic anhydrase isozyme IX (CA IX), an N-glycosylated membrane-associated glycoprotein slas known as the MN or G250 tumour-associated antigen. The invention relates to compositions and methods useful in inhibiting CA IX+ preneoplastic or neoplastic cells. The inhibitors are especially antagonistic anti-CA IX antibodies and other inhibitory agents that target the carbonic anhydrase activity of CA IX on these cells. The antibodies, or their antigen-binding fragments, are specifically reactive such an inhibitory editor of CA IX. Screening assays for identifying such inhibitory agents are provided. The antibodies, their antigenbinding fragments, and other inhibitory agents are useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment of cancers characterised by the expression of CA IX, such as: head and neck cancers; gynaecological cancers including ovarian, cervical, vaginal, endometrial and vulval cancers as well as gynaecological precancerous conditions such as metaplastic cervical tissues and condylomas; gastrointestinal cancers such as stomach, colon and oesophageal cancers; urinary tract cancer such as bladder and cancers; skin cancer; luver cancer; prostate cancer; lung cancer; and
                                                                                                                                                                                                                                                                 combining
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Human carbonic anhydrase IX coding sequence
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22-JUL-2003; 2003US-0489473P.
28-OCT-2003; 2003US-0515104P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating mammal for pre-cancerous or cancerous disease such as head and neck cancer, involves administering composition comprising compound such as inhibitors of MN/carbonic anhydrase IX enzymatic activity to mammal.
                                                                                                                                                                                                                            ds; gene; cytostatic; cancerous disease; carbonic anhydrase IX protein; gene therapy; anticancer; tumor imaging; scintigraphy; necinoma; head and neck cancer; mesodermal tumor; neuroblastic disease; carcinoma; head and neck cancer; mesodermal tumor; neuroblastoma; retinoblastoma; osteosarcoma; Ewing's sarcoma; melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pastorek J;
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13. .1392
/*tag= a
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GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a new isolated polynucleotide (a Human kidney tumour specific cDNA) comprising any one of the 1855 sequences identified in the specification for their complements, degenerate variants, sequences sequences consisting of at least 20 contiguous residues them, sequences that hybridise to them under highly stringent conditions or sequences having at least 75 or 90% sequence identity to the 1855 sequences. Also included are detecting/determining the presence of cancer in a patient, stimulating an immune response in a patient; treating kidney cancer in a patient, an isolated polypeptide encoded by one of the 1855 sequences, an expression vector comprising the polynucleotide operably linked to an
                                                                                                                                                              400
                                                                                                                                                                                                                                                                                                GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotides and polypeptides, useful for detecting the presence of, and treating cancer, particularly kidney cancer by stimulating T-cells specific for a tumor protein, and stimulating immune response in a patient.
                                                                                                                                                                                                                                                                                                                                                                                  AGGGGAACCAAAGGGGGTGTGAGCTACCGCCCAGCAGAGGTAGCCGAGACTGGAGCC 1389
                                                                                                                                                                                                                                                                                                                                                               ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
                                                   ATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCCAGCTCCACACCCTCTCT
                                                                                            AspThrieuTrpGlyProGlyAspSerArgieuGlnLeuAsnPheArgAlaThrGlnPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; 88; kidney tumour; kidney cancer; cytostatic; gene therapy;
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21-DEC-2001; 2001US-0343340P
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vector, an isolated antibody (or its antigen-binding fragment) that specifically binds to the protein, a fusion protein comprising at least one the proteins, stimulating and/or expanding T-cells specific for a tumour protein, an isolated T-cell population comprising at least composition comprising a first component (such as a carrier or immunositualant) and a second component (comprising one of the proteins) and second component (comprising one of the polypeptides, an antibody, T-cell or an antibody presenting cell that expresses the polymucleotide) and a diagnostic kit comprising at least one of the oligonucleotides, or at least one antibody and a detection reagent comprising a reporter group. The polymucleotides, on an ippoptides, and intenting cancer, particularly kidney cancer by stimulating and/or expanding T-cells specific for a tumour protein, and stimulating immune response in a patient. The present sequence is one of the Human kidney tumour specific cDNAs. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence. Use the sequence. The sequence cancer by use obtained in electronic format directly from USPTO at sequence.
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The invention describes a new isolated polymucleotide (I) comprising: any one of the 1855 sequences identified in the specification; complements or degenerate variants of (a); sequences consisting of at least 20 contiguous residues of (a); sequences that hybridize to (a) under highly stringent conditions; or sequences that hybridize to (a) under highly stringent conditions; or sequences having at least 75 or 90% sequence identity to (a). Also described are: detecting (M1) or determining the presence of cancer in a patient; attimulating (M2) an immune response in a patient; treating (M3) kidney cancer in a patient; an isolated or polypeptide (II) enrocded by (I) and comprising, or having at least 70 or 90% sequence identity to, any one of the 8 sequences identified in the specification; an expression vector (III) comprising (I) operably linked to an expression control sequence; a host cell (IV) transformed or transfected with (III); an isolated antibody (V) or its antigen-binding fragment that specifically binds to (II); a noligonucleotide (VII) that hybridizes to the nucleotide sequences cited above under highly stringent conditions; stimulating (M4) and/or expanding T-cells specific for a tumor protein; an isolated T-cell spulling the T-cells in (M4); a comprising at least one (II) comprising the T-cells in (M4); a composition (IX) comprising a first component such as a carrier or immunostimulant and a second component such as a carrier or immunostimulant and a second component comprising (I), the polymetric specifically binds to (II), (VI), or an antigen-presenting cell that specific and a diagnostic kit (X) comprising at the plagnoutle comprising a feet to expresses the polymucleotide, or at least one of the polymucleotide, or at least one of the presence of, and treating cener, particularly kidney tumour cDNN, expression of which is increased in concer by stimulating and vor expanding T-cells specific for a tumor concern, and stimulating and energence of a patient. This sequence of the concern of the concer
                                                                                                                                                                              New isolated polymucleotides and polypeptides, useful for detecting the presence of, and treating cancer, particularly kidney cancer by stimulating T-cells specific for a tumor protein, and stimulating immune response in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1519 BP; 296 A; 456 C; 453 G; 314 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                          Gordon B,
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                                                                                             Gaiger A,
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21-DEC-2001; 2001US-0343340P.
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Query Match:
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20 69

10 AIGGCTCCCCTGTGCCCCCAGCCCTGGCTCCCTCTTTGATCCCGGCCCCTGCTCCAGGC

Met Ala ProLeu Cys ProSer ProTrpLeu ProLeu Leu Ile Pro Ala Pro Ala Pro Gly

US-09-967-237B-2 (1-459) x ADW41952 (1-1519)

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41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGluAspAspProLeu

70 CTCACTGTGCAACTGCTGCTGCTGCTGCTTCTGATGCCTGTCCCATCCCCAAGGTTG

21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu

GlyGluGluAspLeuDroSerGluGluAspSerProArgGluGluAspProProGlyGlu

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MN gene, protein and nucleic acid fragments - used as primers and probes in the detection of MN antigens and antibodies, and in the treatment of (pre) neoplastic disease.
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                                                                                                                                                                                                                                              MuTu; endogenous; cellular component; MN; HeLa cell; diagnosis; lymphocytic choriomeningitis virus; LCMV; putative oncogene; treatment; neoplastic; pre-neoplastic; disease; antisense therapy; antibody; vaccine; vertebrate; immunisation; ss.
             Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;
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95US-00477504.
95US-00481658.
95US-00485049.
95US-00485862.
                                                                                                           AAT09186 standard; cDNA; 1522
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P-PSDB; AAR88058.
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19-AUG-1996
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                            GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro
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                                                                                                                                                      AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe
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95US-0047504.
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P-PSDB; AAY53228.
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30-DEC-1993;
15-JUN-1994;
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The present invention describes a method of screening for preneoplastic/neoplastic disease. The method comprises: (1) determining whether abnormal MW gene expression is present in a vertebrate; and (2) if abnormal MW gene expression is determined to be present in the vertebrate, determining that the vertebrate has a significant risk of having preneoplastic/neoplastic disease. The MW gene is an oncogene and encodes an MW protein (also referred to as MW/CA IX isoenzyme). The MW protein is a tumour associated carbonic anhydrase isoenzyme. The method is used for detecting a wide variety of preneoplastic/neoplastic diseases in a vertebrate, preferably a human. The disease detected is mammary. bladder, renal, urinary tract, ovarian, uterine, cervical, endometrial, vapinal, valual, prostate, liver, lung, skin, thyroid, pancreatic, testicular, brain, head and neck, mesodermal, gallbladder, rectal, duodenal, jejunal, ileal, gastric, pancreatic duct, liver duct, gastric mucosa, gallbladder epithelium, small intestinal mucosa, colorectal mucosa, pancreatic disease. AAAA6540 to AAA16617 and AAY53228 to AAY5345 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention
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Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;

	20	40	60	80 252	100 312	120 372	140 432	160 492	180 552	200	220
Length: 1522 Matches: 459 Conservative: 0 Mismatches: 0 Indels: 0 Gaps: 0	MetalaProLeuCysProSerProTrpLeuProLeuLeuIleProAlaProAlaProGly 2	LeuThrValGlnLeuLeuLeuSerLeuLeuLeuLeuMet ProValHisProGlnArgLeu 4	ProArgMetGlnGluAspSerProLeuGlyGlyGlyGlySerSerGlyGluAspAspProLeu 6	GlydludluaspleuProSerGluGluAspSerProArgGluGluaspProProGlyGlu 8 	GluaspLeuProGlyGluGluaspLeuProGlyGluGluaspLeuProGluValLysPro 1 	LysserGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 1 	AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 1 	TrpargTyrGlyGlydBroProTrpProArgValSerProAlaCysAlaGlyArgPhe 1 	GINSerProValAspIleArgProGInLeuAlaAlaPheCysProAlaLeuArgProLeu 1	GlubeuleudlypheGlubeuProProbeuProGlubeuArgbeuArgAsnAsnGlyHis 2	SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 2
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                                                GTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGCACCGCCTTTGCC
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                                   ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThr
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13. .1392
/*tag= a
/product= "Human MN protein"
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The invention relates to the inhibition of cell adhesion mediated by the MN oncoprocein (also known as the MN/CA IX isoenzyme or the MN/C250 MN oncoprocein (also known as the MN/CA IX isoenzyme or the MN/C250 protein). The MW protein is a tumour-associated adhesion molecule which comprises a proteoglycan-like (PG) domain (AAB03017) which contains the protein's binding site, and a carbonic anhydrase (CA) domain (AAB03018). Abnormal expression of the MN protein is associated with tumorigenicity. The invention encompasses molecules (e.g., proteins and peptides) which which specifically bind to a site on the MN protein and peptides) which concompasses MN protein fragments which can be addeed to the extracellular environment to prevent the adhesion of vertebrate of also encompasses MN protein or MN protein fragments which can be addeed to the extracellular environment to prevent the adhesion of vertebrate or also encompasses in the protein and to a method of identifying a site of the binding site of the MN protein in a cell adhesion assay. The coverlapping peptides from the protein in a cell adhesion assay. The invention encompasses a vector comprising testing a series of coverlapping peptides from the protein in a cell adhesion assay. The invention encompasses a vector comprising the variable domains of a NN-specific antibody, where the domains are separated by a flexible compression. The invention also encompasses a vector comprising a nucleic acid encoding a cytocoxic protein or peptide operatively linked to the MN complastic cell that abnormally expresses MN gene promoter. Which inhibites the growth of a vector comprising a nucleic acid encoding a cytocoxic protein or peptide operatively linked to the MN gene promoter. Which inhibites the growth of a vector comprising and expresses of cand peptides, MN-binding proteins and peptides, MN-binding proteins and peptides. The present sequence (e.g., cancers) associated with or characterised by abnormal MN protein represent sequence represent represented and peptides.
                                                                                                                                                                                                                                                                                                                                                                                    A molecule which specifically binds to a site on MN protein (oncoprotein) and prevents adhesion of vertebrate cells to the protein, useful for treating preneoplastic or neoplastic diseases such as cancer.
                                                                                                                                                                                                                                                                 Pastorek J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 1A-C; 154pp; English.
                                                                       99WO-US024879
                                                                                                                  98US-00177776
98US-00178115
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                                                                                                                                                                                          (FARB ) BAYER CORP.
(VIRO-) INST VIROLOGY.
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P-PSDB; AAB03005.
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0 U; 0 Other; 1522 459 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: 453 G; 314 T; Gaps: BP; 297 A; 458 C; 1.85e-130 2424.00 100.0% 100.0% Similarity: Percent Similarity:

US-09-967-237B-2 (1-459) x AAA52459 (1-1522)

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1212 1032 1092 GACACCCTGTGGGGAACCTGGTGACTCTCGGCTAACATGTTCCGAGCGACGCCACT 1152 280 240 PheSerargTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380 400 GluhapLeuProGlyGluGluhapLeuProGlyGluGluhapLeuProGluValLyaPro 100 372 140 432 160 492 200 612 220 672 732 260 792 912 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420 252 312 120 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180 552 852 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300 192 TTGAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGAGTGGACAGCAGTCCTCGGGCT 913 GAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTCCTGCCCTCTGAC AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis Gregaageccaccerrrecergecgagarecacgregrreacereacaccerrrece AGAGTTGACGAGGCCTTGGGGCGCCCGGGAGGCCTTGGCCGTGTTGGCCGCCTTTCTGGAG GAGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTGGAAGAAATCGCT rrcagccgcracrrccaarargagggrcrcrcacracaccgcccrgrgrcccaggrgrc ATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGCTCCACACCCTCTCT 133 CCCGGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAAGATGACCCACTG GAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAAGTTAAGCCT LysSerGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly GATCCTCAAGAACCCCAGAATAATGCCCACAGGGGACAAAGAAGGGGGATGACCAGAGTCAT TrpArgTyrGlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe CAGTCCCCGGTGGATATCCGCCCCCAGTCGCCCGCCTTCTGCCCGGCCCTGGGCCCCTG GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnAsnGlyHis SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThr ArgValAspGluAlaLeuGlyArgProGlyGlyEeuAlaValLeuAlaAlaPheLeuGlu LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 61 GlydludluAspLeuProSerGludluAspSerProArgGluGluAspProProGlyGlu ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 313 373 493 673 793 853 321 1033 361 1093 381 81 101 121 141 161 181 553 201 613 221 241 733 261 281 301 973 ò 8 g ð 셤 8 셤 à a ઠે 셤 à 셤 è 셤 ò ద ሯ 셤 ઠે 요 ò 셤 ઠે g ò В ð 셤 8 요 8 용 8

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This invention relates to a novel monoclonal antibody identified as the MN/CA IX specific antibody prepared in knockout mice (CA IX deficient mice). Specifically, this antibody is directed trowards the MN gene, a cellular oncogene known alternatively as carbonic anhydrase 9, CA9 or MN/CA9, which encodes the MN protein that is also known as the MN/CA IX is obenixyme, carbonic anhydrase IX, CA IX or the MN/G250 protein. The present invention describes the generation of this monoclonal antibody, and immunoreactive fragments thereof, which are directed against non-cantibody can be useful diagnostically as a marker for preneoplastic/ nooplastic tumours, immunodetection methods and immunoracgeting captroaches. Accordingly, compositions exhibit cytostatic activity and are useful in the diagnosis, prognosis and treatment of various cancers including breast, bladder or lung cancer, in tumour therapy and in antibuton in the diagnosis or includence is the human MN cDNA of
GECCTCCTTTTTGCTGTCACCAGCGTCGCGTTCCTTGTGCAGATGAGAAGCAGCACACAA 1332
                                                                                                    GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
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GACACCCTGTGGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGAGCGACGCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New soluble form of the carbonic anhydrase IX (CA IX) protein for screening, diagnosing or prognosing diseases associated with abnormal expression of CA IX protein, e.g. renal cell carcinoma, breast cancer
                                                                                                                                                                                                                          GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg
                                                                                 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro
                                                                                                                              LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla
                                                                                                                                                                            AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                      carbonic anhydrase IX; CA IX; precancerous cell; MN; cancerous cell;
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renal cell carcinoma; breast cancer; colorectal cancer; ds; gene.
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IX (CA IX) (or MN) protein or CA IX polypeptide which is released from precancerous and/or cancerous cells of a vertebrate into a body fluid. The invention may be useful for the development of compounds with a cytostatic activity or a vaccine whilet the disclosed sequences may be used for gene therapy. The protein and method are useful for screening, diagnosing or prognosing diseases associated with abnormal expression of carbonic anhydrase IX protein, such as precancerous and cancerous diseases like renal cell carcinoma, breast cancer or colorectal cancer. The monoclonal antibody may also be used for treating or precenting precancerous and cancerous diseases. The present sequence is that of the gene which encodes the human MN protein of the invention.
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Pastorek

Zavada J,

Pastorekova S,

Rocken C,

Ebert M,

18-OCT-2004; 2004WO-US034573 16-OCT-2003; 2003US-0511832P (FARB) BAYER HEALTHCARE. (VIRO-) INST VIROLOGY.

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                                        Prognosis; oncogene; neoplasm; MN/CA IX; stomach tumor; gallbladder disease; biliary cancer; biliary tumor; testis tumor; ovary tumor; basal cell carcinoma; central nervous system tumor; gene;
GTGGAAGGCCACCGTTTCCCTGCCGACATCCACGTGGTTCACCTCACGTGCTTTGCC
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                                                                                                 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla
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/product= "Mature MN/CA IX"
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The invention relates to a method of prognosticating a preneoplastic/neoplastic disease afflicting a subject vertebrate, where preneoplastic/neoplastic disease afflicting a subject vertebrate, where the disease affects a tissue that normally expression upon but loses or has significantly reduced MN/CAA IX expression upon carcinogenesis, comprising detecting an MN/CAA gene expression product in the sample, comparing the level of the MN/CAA gene expression product to in the sample, comparing the level of MN/CAA gene expression product to the average level of MN/CAA gene expression product to the average level of MN/CAA gene expression product to the average level of MN/CAA gene expression product to the average level of MN/CAA gene expression product to the average level of MN/CAA gene expression product to the average level of MN/CAA gene expression product disease as the subject vertebrate, and determining that the subject vertebrate has a poorer prognosis if the level of MN/CAA gene expression product quantitated is higher than the average level of MN/CAA gene expression product in the comparable samples. The methods and compositions of the present invention are useful in medical genetics, biochemical engineering, immunochemistry and oncology, in particular for prognosticating preneoplastic/neoplastic diseases of gastric mucosa, gallbladder, biliary ducts, ductal cells of duodenal glands, testis and celevary, basal cells of hair follicles and central nervous system choroid plexus. This sequence represents cDNA
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                                                                                                                                                                                                                                                     Prognosticating preneoplastic/neoplastic diseases of the breast, gallbladder, biliary ducts, testis or ovaries, by detecting MN/CA9 gene expression products, useful in medical genetics, biochemical engineering
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Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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Lung cancer related gene sequence SEQ ID NO:3116
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Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

English Claim 1; SEQ ID NO 3116; 44pp;

The present invention describes a method (MI) for screening for an antinoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in AB161664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating lobular cancer, aguamou

Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

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Š i	281	GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300
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& a	301 943	GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuFroSerAsp 320
ò	321	PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340
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X 23 3	Colon ad	enocarcinoma related gene sequence SEQ ID NO:516.
\$ \$ \$ \$ \$ \$		Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma; gene; ds.
X 8 X	Homo sapi	ens.

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properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophagaal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clar cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Milm's
                                                                            Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
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The present invention describes a method (M1) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent expession of anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 expression is indicative of smith-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producting a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or

Claim 1; SEQ ID NO 516; 44pp; English

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Percent Similarity:
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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                  GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla
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The present invention describes a method (M1) for screening for an antinoplastic agent. The method involves exposing cells to a chemical agent copplastic agent. The method involves exposing cells to a chemical agent cobe tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 comprises in at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity, and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is anti-neoplastic agent. And can be used for producing a product which is connected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, ossophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
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2000US-0236842P.
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2000US-0237172P.
2000US-0237172P.
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2000US-0235638P.
2000US-0235711P.
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2000US-0235863P.
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Length:
Matches:
Conservative:
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Indels:
Gaps:

1.88e-130 2424.00 100.0% 100.0% 100.0%

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02-OCT-2000; 2000US-0237173P.
02-OCT-2000; 2000US-0237278P.
02-OCT-2000; 2000US-0237295P.
02-OCT-2000; 2000US-0237316P.
03-OCT-2000; 2000US-0237316P.
03-OCT-2000; 2000US-023759P.
03-OCT-2000; 2000US-0237604P.
03-OCT-2000; 2000US-0237606P.
03-OCT-2000; 2000US-0237606P.
01-NOV-2000; 2000US-0244867P.
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102 162 222 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100 40 9 80 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu ATGGCTCCCCTGTGCCCCCAGCCCCTGGCTCCTCTGTTGATCCCGGCCCCTGCTCCAGGC CTCACTGTGCAACTGCTGCTGTCACTGCTTCTGATGCCTGTCCATCCCCAGAGGTTG ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGluAspAspProLeu cecedargeagarrececrregaagaereriereaagaererreregagaagareaere GGCGAGGAGGATCTGCCCAGTGAAGAGATTCACCCAGAGAGGAGGATCCACCCGGAGAG MetAlaProLeuCysProSerProTrpLeuProLeuLeuIleProAlaProAlaProGly LeuThrValGlnLeuLeuLeuLeuLeuLeuLeuLeuMetProValHisProGlnArgleu 1552 459 0000 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: (1-1552)x ABL68346 1.88e-130 2424.00 100.0% 100.0% US-09-967-237B-2 (1-459) Best Local Similarity: Query Match: DB: Percent Similarity: Alignment Scores: Pred. No.: 21 43 103 41 163 61

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1122 1182 1242 TTCAGCCGCTACTTCCAATATGAGGGGTCTCTCACTACACCGCCCTGTGCCCAGGGTGTC 1062 GCTGAGCCAGTCCAGCTGAATTCCTGCCTGGCTGCTGACATCCTAGCCCTGGTTTTT 1302 esecrecriririscrercaccaccarcecrirerrerscagardadededededada 1362 440 140 380 320 340 360 400 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420 342 120 402 462 160 522 180 582 200 642 220 702 240 762 260 822 280 882 300 942 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu CAGTCCCCGGTGGATATCCGCCCCCAGCTCGCCGCCTTCTGCCCGGCCCTGCGCCCCTG ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla TrpArgTyrGlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe GTGGAAGGCCACCGTTTCCCTGCCGACATCCACGTGGTTCACCTCAGGACCGCCTTTGCC GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla GACACCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTTCCGAGCGACGCCG GAGGATCTACCTGGAGGAGGATCTACCTGGAGGAGGATCTACCTGAAGTTAAGCCT GATCCTCAAGAACCCCCAGAATAATGCCCACAGGGGCACAAAGAAGGGGGATGACCAGAGTCAT GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnAsnGlyHis GAACTCCTGGGCTTCCAGCTCCCGCCGCTCCCAGAACTGCGCCCTGCGCAAAAAAGGCCAC SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThr CGGGCTCTGCAGCTGCATCTGCACTGCGGGGCTGCAGGTCGTCCGGGCTCGGAGCACA ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla GAGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTGGAAGAAATCGCT GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp LysSerGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly reacecraredadeceacceccecceccecesererececaecerecedecececerre PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 1063 381 1303 343 141 523 583 1003 1123 1183 1243 121 403 463 161 181 221 703 241 763 261 823 281 883 943 341 361 401 421 283 101 201 301 321

Similarity:

Local

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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits in increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated polypeptide, for cancer in a patient and for treating a mammal having lung cancer in a patient and for treating a mammal having lung cancer for other benign or precancerous lesions, e.g. atelectasis, lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful compounds that modulate lung cancer, such as antibodies. Sequences of ABX76124-ABX76474 represent lung cancer, such as articled polynucleotides of the
                                                                                                                                                                                                                             Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lession; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
1363 AGGGGAACCAAAGGGGGTGTGAGCTACCGCCCAGCAGAGGTAGCCGAGACTGGAGCC 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased
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10-MAY-2001; 2001US-0290492P.
09-NOY-2001; 2001US-0339245P.
29-NOY-2001; 2001US-0350666P.
29-NOY-2002; 2001US-034370P.
12-APR-2002; 2002US-0372246P.
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P-PSDB; ABU56656.
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1552 459 0

Length: Matches: Conservative:

1.88e-130 2424.00 100.0%

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GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla
                                                                   845 GAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTGGAAGAAATCGCT
                                                                                                                                                                           PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Farday Avenue
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1 (bases 1 to 1523)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (B-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                    CRS97234 110-100 1541 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DI085YF18 of Placenta Cot 25-normalized of Homo sapiens (human).
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 1541)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Lil, W.B., Gruber, C. Jessee, J. and Polayes, D.

Unjull-length cDNA libraries and normalization

Unpublished
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/organism="Homo sapiens"
/mol_type="mkNa"
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/clone="CSODI085YF18"
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458
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                   3.07e-185
2420.00
100.0%
99.8%
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Best Local Similarity:
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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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CR590646.1 GI:50471453
HTC; CNSLT_CDNA.
HTC; CNSLT_CDNA.
HTCHOMO sapiens (human)
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1. (bases 1 to 1492)

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1. W. Gruber, C., Jessee, J. and Polayes, D. Pull-length cDNA libraries and normalization
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="csobJ005YK14"
/tissue_type="T_cells (Jurkat_cell line)
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Conservative: 1
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/tissue_type="Placenta
/plasmid="pCMVSPORT_6"
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1 (bases 1 to 1380)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Whies,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
(er) PLoS Biol. 3 (6), E170 (2005)
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Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B. Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B. Nielsen, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 200550, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
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                                                                                                                 TIGAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGAGTGGACAGCAGTGCTCTCGGGCT
                                           PheserargTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal
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1. 1380
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/db_xref="texon:9606"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DQ049266 1380 bp
Homo sapiens CA9 gene, VIRTUAL TRA
genomic survey sequence.
DQ049266 1G1:66902465
DQ049266.1 GI:66902465
Homo sapiens (human)
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/gene="CA9"
/locus_tag="HC17258"
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231 Phesenhily(Phesdimyrcludiyserlauffill(ORIGIN Alignment Scores: 2.68e-145 Length: 1380 Score: 1926.00 Matches: 385
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1 6; 1st strand cDNA was primed

Imer. Five prime end enriched,
ligested with Not I and cloned into
is of the pCMVSPORT 6 vector.
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91057 BVRX cedex - FRANCE
10b : www.genoscope.cns.fr
NotI-oligo(dT) primer. Five prime
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                       GlnLeuhanPheArgAlaThrGlnPro 380
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s; Primates; Catarrhini;
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Hominidae; Homo.

Hominidae; Homo.

It (bases 1 to 1070)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31276515.

Contact: Genoscope

Genoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage

Z rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                 AL554705 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA COT 25-NORMALIZED Homo sapiens CDNA COD CSODIO85YP18 5-PRIME, mRNA sequence.
/organism="Homo sapiens"
/organism="Homo sapiens"
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/clone="CSODIO85YP18"
/clone="CSODIO85YP18"
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/clone lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/note="Ist strand cDNA was primed with a Not1-oligo(dT)
/primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized."
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BST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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Matches:
Conservative:
Mismatches:
Indels:
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us-09-967-237b-2.rst

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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31280177.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCWVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                            For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODJ005BF07QP1&c=5300.f. Location/Qualifiers
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       REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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                        GluaspLeuProGlyGluGluaspLeuProGlyGluGluaspLeuProGluValLysPro
                                                                                                                  LysSerGluGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly
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          GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu
                                                                                        GAGGATCTACCTGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCTGAAGTTAAGCCT
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1. .1009

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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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311
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                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                      1.44e-115
1556.50
97.8%
97.8%
64.2%
                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                        Alignment Scores:
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AL558378 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED Homo sapiens CODJ005YK14 5-PRIME, mRNA sequence.
AL558378 3 GI:46183776

DEFINITION

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.

Homo sapiens (human) Homo sapiens

ACCESSION VERSION KEYWORDS SOURCE ORGANISM >

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ProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAlaGluGlu 302
/note="lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime and enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ScoR V sites of the pcMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGGAAGATGACCCACTGGGCGAG
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290
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                       4.13e-111
1501.50
93.0%
92.4%
61.9%
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                                                                                                                                                            Percent Similarity:
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On May 13, 2003 this sequence version replaced gi:30626393.
On May 13, 2003 this sequence version replaced gi:30626393.
Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                  /organism="Homo sapiens"
/mol_type="mRNN3"
/mol_type="mRNN3"
/clone="CSODKO09YP10"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA CELLS"
/cell_line="HELA CELLS"
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     TGGCGCTATGGAGGCGACCCGCCCTGGCCCCCGGGTGTCCCCCAGCCTGCGCGGGCCGCTTC
                                                                                                         GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnAsnGlyHis
                                                                                                                             GAACTCCTGGGCTTCCAGCTCCCGCTCCCAGAACTGCGCCTGCGCCAACAATGGCCAC
                                                                                                                                                                            SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae, Homo.

1 (bases 1 to 1017)

Li, W. B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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LysSerGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
1 (bases 1 to 971)
Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
Proll, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CO579387 CO 50239 Katze MAIL Macaca mulatta cDNA clone IBIUW:17608 57 similar to Bases 6 to 971 highly similar to human CAS (He.63287), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu
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                     GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu
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Analysis of the Macaca mulatta transcriptome and the sequence
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/tissue type="NEWROBLASTOWA"
/clone lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, wolble-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCWVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies,
division of Invitrogen.
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                     911
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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Metala ProLeuCys ProSer ProTrp Leu ProLeu Leu Ile ProAla ProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence belongs to sequence cluster 5300.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CSIDA001ZF090P1&c=5300.f.

Location/Qualifiers
                                                                                                                                                                  BX423970

916 bp mRNA linear EST 03-NEX423970 Homo sapiens CDNA clone CS0DA003YB12 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                      Hominidae, Homo.

1 (bases 1 to 916)

1 (bases 1 to 916)

1 (law B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 15, 2003 this sequence version replaced gi:30766328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
                                                        GlySerGluThrGlnValProGlyLeuAspIleSerAlaLeu 316
                                                                                          GGT---CAGAGMTCAAGTCCAGGACTGGAMTAYTGCVTYCTG 950
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Matches:
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/mol_type="mRNA"
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90.8%
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Hominidae; Homo.

1. (Dases 1 to 927)

1. (Dases 1 to 927)

2. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

1. Full-length cDNA libraries and normalization

1. Unpublished (2001)

1. On Feb 15, 2001 this sequence version replaced gi:31276993.

1. Contact: Genoscope

Genoscope - Centre National de Sequencage

2. rue daston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL555184 BY SAPENDE BY DE WRNA linear EST 30-MAR-2004 AL555184 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens CDNA clone CSODK007XK10 5-PRIME, mRNA sequence.

AL555184.3 GI:45859924 EST.
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                274 lreualaalaPhereuGluGluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AlaCysAlaGlyArgPheGlnSerProValAspIleArgProGlnLeuAlaAlaPheCys 174
                                                                                                                            Email: cmagness@illumigen.com
Sequenced on 2004.07.15. 725 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org
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                                                                             USA
                                                                             Seattle, WA 98134,
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Matches:
Conservative:
Mismatches:
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BACKWARD: CACTATAGGGCGAATTGGGTA
Insert Length: 971 Std Error: 0.00
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                                                                         2203 Airport Way S, Suite 450,
Tel: 2063780400
Fax: 2063780408
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Contact: C. Magness
Illumigen Biosciences Inc
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1452.50
88.9%
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AGENCOURT_51019039 DFCI-Vidal horfeome 1.1 Homo sapiens CDNA clone IMAGE:40030000 5', mRNA sequence.
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1 (bases 1 to 830)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                  Office of Cancer Genomics (No. 1).

Office of Cancer Genomics (No. 1).

Bidg. 31 Ran10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov
Tissue Procurement: Marc Vidal

CDNA Library Preparation: Dana Farber Cancer Institute/Vidal Lab

CDNA Library Preparation: Dana Farber Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:

http://image.llnl.gov column: 01

High quality: sequence stop: 712.
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1. 830
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHisTrpArg 142
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primer. Five prime end enriched, double-strand cDNA was
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sites of the pCMVSPORT 6 vector. Library was normalized.
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The Wellcome Trust Sanger Institute
Genome Campus, CBIO 1SA, UNITED KINGDOM
Merozoite CDNA library: Frank Katzer and Brian Shiels, Division of
Veterinary Infection and Immunity, ICM, University of Glasgow, UK.
Location/Qualifiers
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/clone lib="Theileria annulata me/note="country: Turkey:Ankara"
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S Pain, A., Renauld, H., Berriman, M., Murphy, L., Yeats, C.A., Weir, W., Kerhornou, A., Rabett, M., Bishop, R., Bouchier, C., Cochet, M., Coulson, R.M.R., Cronin, A., de Villiers, E., Fraser, A., Fosker, N., Gardher, M., Goble, A., Griffiths-Jones, S., Harris, D.E., Katzer, F., Iarke, N., Lord, A., Maser, P., McKellar, S., Mooney, P., Morton, F., Nene, V., O'Neil, S., Price, C., Quail, M.A., Rabbinowitsch, E., Rawlings, N.D., Rutter, S., Saunders, D., Seeger, K., Shah, T., Squares, R., Squares, S., Tivey, A., Walker, A.R., Woodward, J., Dobbelaer, D.A.B., Langsley, G., Rajandream, M.-A., McKeever, D., Shiels, B., Tait, A., Barrell, B. and Hall, N.

The genome of the host-cell transforming parasite Theileria annulate and a comparison with T. parva

Unpublished (2005)

Contact: Pain A

The Pathogen Sequencing Unit
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                                               GGCGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGATCCACCCGGAGAG
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS REFERENCE

JOURNAL COMMENT

DEFINITION AJ924825 LOCUS

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CHAIN MINE TO BE SHIP

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Run on:

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11913, A 16074, A 5, Appli 28, Appli

Sequence 5 Sequence 5 Sequence 2 Sequence 2

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COMPUTER TEADBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRICA APPLICATION NUMBER: US 08/260,190
FILING DATE: LS-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                       US-09-949-016-4332

US-09-949-016-4332

US-08-35-469-11

US-08-260-190-23

US-08-35-469-11

US-08-35-469-11

US-08-36-016-11913

US-09-949-016-11913

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US-08-481-658B-49
US-08-477-504A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
APPLICANT: Pastorek, Jaromir
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
STREET: 6 Mariposa Court
CITY: Tiburon
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1, Application US/08481658B
; Patent No. 5955075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lauder, Leona L.
REGISTRATION NUMBER: 3
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-Q=/abss/ABSSWEB_spool/US09967237/runat_15022006_182246_28055/app_query.fasta_1
-Q=/abss/ABSSWEB_spool/US09967237/runat_15022006_182246_28055/app_query.fasta_1
-DB=Issued Patente NA -OPMT-fastap -SUFFIX=rni -MINNATCH=0.1 -LOOPGI=0
-LOOPEXT=0 -UNITS=bits -START=1 -BND=-1 -MATRIX=blosum62 -TRNNS=human40.cdi
-LOST=2 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGARDP=10 -XGARDEXT=0.5 -FGAPOP=6
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                                                                                                                                                               US-09-967-237B-2
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1 MAPLCPSPWLPLLIPAPAPG......RRGTKGGVSYRPAEVAETGA 459
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Sequence 1,
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Sequence 1,
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                 GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_NA:*

1. /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2. /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4. /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/PG_COMB.seq:*

7. /cgn2_6/ptodata/1/ina/PG_COMB.seq:*

7. /cgn2_6/ptodata/1/ina/PC_COMB.seq:*

8. /cgn2_6/ptodata/1/ina/PC_COMB.seq:*

9. /cgn2_6/ptodata/1/ina/RE_COMB.seq:*

9. /cgn2_6/ptodata/1/ina/RE_COMB.seq:*

9. /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
                                                                            nucleic search, using frame_plus_p2n model
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US-08-486-756A-1
US-08-486-756A-1
US-08-787-739-1
US-08-487-077A-1
US-08-485-663A-1
US-08-485-043D-1
US-09-178-115-1
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Perfect score:
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Result No.

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Sequence 28, Sequence 49, Sequence 49,

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| IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360
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                                                                                                GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300
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                                                                                                                                                                     793 AGAGTTGACGAGGCCTTGGGGCGCCCGGGAGGCCTGGCCGTGTTGGCCGCCTTTCTGGAG
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                                            ArgvalAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPC
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION A124
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08477504A
; Sequence 1, Application US/08477504A
; Patent No. 597253
; GENERAL INFORMATION:
    APPLICANT: Zavada, Jan
    APPLICANT: Pastorekova, Silvia
    APPLICANT: Pastorek, Jaromir
    TITLE OF INVENTION: MN Gene and Protein
    NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
    ADDRESSE: Leona L. Lauder
    STRET: 6 Mariposa Court
    CITY: Tiburon
    STATE: California
    COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                   Length:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Best Local Similarity:
Query Match:
DB:
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HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
US-08-481-658B-1
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Pred. No.:
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1033 ATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGCTCCACACCCTCTCT 1092
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                        241 ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla
                                         853 GAGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTGGAAGAAATCGCT
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ZIP: 05A

ZIP: 49420

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-08-486-756A-1
; Sequence 1, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
    APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
STRER: Galantiposa Court
CITY: Tiburon
STATE: California
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Matches:
Conservative:
Mismatches:
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NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REPERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-034
TELEPHONE: 415-435-0727
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNES: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
HYPOTHETICAL: NO
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2424.00
100.0%
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Best Local Similarity:
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Pred. No.:
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US-08-477-504A-1
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                     221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThr
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MEDIUM TYPE: Floppy disk
COMPUTER: ISH PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/485,862B
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APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Leona L. Laude
STREET: 6 Mariposa Court
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CITY: Tiburon
STATE: California
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Matches:
Conservative:
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APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-UN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
TELEPHONE: 415-435-2034
TELEPHONE: 415-435-0727
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                  7.5e-197
2424.00
100.0%
100.0%
                                                                                                                                                                           LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                      ; ANTI-SENSE: NO
US-08-486-756A-1
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Pred. No.:
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                           201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr
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APPLICANT: Pastorekva, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Prot
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSER: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
CITY: San Francisco
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104
CONFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08787739; Patent No. 6027887; GENERAL INFORMATION:
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Matches:
Conservative:
Mismatches:
Indels:
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           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY AGENT INFORMATION:
NAME: LANGEY, LEGNA L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELEPHONE: 415-435-2034
TELEPHONE: 415-435-2034
TELEPHONE: 415-435-2034
TELEPHONE: 415-435-2037
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDRESS: single
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2424.00
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                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
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                               LysSerGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CUBRENT APPLICATION DATA:
PFLING DATE: 24-JAN-1997
FILING DATE: 24-JAN-1997
PRIOR APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/485,063
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
TELEPRAK: 415-981-0334
TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERSTICE:
FURDERAL INFORMATION:
FELLERAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERSTICE:
FURDERAY INFORMATION:
FELLERAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
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2424.00
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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Best Local Similarity:
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Pred. No.:
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81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100
                                                                   ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu
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MEDIUM TYPE: Floppy disk
COMPUTER: ISP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPC
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,077A
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
PRICE APPLICATION DATA:
PRICE APPLICATION NUMBER: US/08/487,077A
APPLICATION NUMBER: US/08/487,077A
APPLICATION NUMBER: US/08/487,077A
APPLICATION NUMBER: US/08/487,077A
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                                                             APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08487077A Patent No. 6069242 GENERAL INFORMATION:
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CITY: Tiburon
STATE: California
COUNTRY: USA
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Best Local Similarity:
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Pred. No.:
             US-08-487-077A-1
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GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu
            LysSerGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly
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                                                                                                                                                                                                                                                        ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
CURRENT APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION: 514
PRIOR APPLICATION: 514
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
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                                                                      Sequence 1, Application US/08485863A
Patent No. 6093548
GENERAL INNORMATION:
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3G
TELECHONE: 415-435-034
TELEPHONE: 415-435-0727
INFORMATION FOR SEG ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDENRES: single
TOPOLOGY: linear
                                                                                                                                                                                             ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
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STATE: California
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Pred. No.:
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                                                                   LeuThrValGlnLeuLeuLeuLeuLeuLeuLeuMetProValHisProGlnArgLeu
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,049D
FILING DATE: 07-070N 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-UN-1994
ATTORNEY/AGENT INFORMATION:
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Matches:
Conservative:
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                                                                                                                   Sequence 1. Application US/08485049D

Sequence I. Application US/08485049D

GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekva, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street
CITY: San Francisco
STATE: California
COUNTRY: USA
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Gaps:
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REGISTRATION NUMBER: 30,863
REPRENCE/DOCKET NUMBER: D-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
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STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity:
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73 CTCACTGTGCAACTGCTGTCACTGCTGCTTCTGATGCCTGTCCATCCCCAGAGGTTG
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                                                                   GGCCTCCTTTTTGCTGTCACCAGCGTCGCGTTCCTTGTGCAGATGAGAAAGCAGCACACAGA 1332
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                                                                                                                                                                                                                               Sequence 1, Application US/09178115
Fatent No. 6297041
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekva, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
FILE REFERENCE: D-0021.5A
CURRENT APPLICATION NUMBER: US/09/179, TG
EARLIER APPLICATION NUMBER: 09/177, 776
EARLIER PILING DATE: 1998-10-23
EARLIER PILING DATE: 1998-10-23
EARLIER PILING DATE: 1999-01-24
EARLIER PILING DATE: 1995-06-07
EARLIER PPLICATION NUMBER: 08/486, 049
EARLIER PILING DATE: 1995-06-07
EARLIER PILING DATE: 1995-06-07
EARLIER PLING DATE: 1995-06-07
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; LOCATION: (124)..(1389)
US-09-178-115-1
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NAME/KEY: CDS
LOCATION: (13)..(1389)
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Best Local Similarity:
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ORGANISM: HUMAN
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US-09-178-115-1
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                             AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro
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eTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PLOC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
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APPLICATION NUMBER: US/09/772,719B
FILING DATE: 30 - 2an-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3A-2
TELEPHONE: 415-981-0334
TELEPHONE: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Leona L. Lauder
STRETT: 465 California Street, Suite
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO: 1:
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Pastorekova, Silvia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-09-772-719B-1
Sequence 1, Application US/09772719B
Patent No. 6770438
GENERAL INFORMATION:
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LENGTH: 1522 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu
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   Length:
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            13 CTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCCTGTCCATCCCCAAGGTTG
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                                                                                                                                                                                    RESULT 12
US-08-260-190-5
Sequence 5, Application US/08260190A
PAPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Jaromir
TITLE NO INVENTION: MN Gene and Protein
FILE REPRENCE: D-0021-2
CURRENT APPLICATION NUMBER: US/08/260,190A
CURRENT FILING DATE: 1994-0-15
EARLIER PILING DATE: 1993-12-30
EARLIER PILING DATE: 1993-12-30
EARLIER PILING DATE: 1993-10-21
EARLIER PILING DATE: 1992-10-21
EARLIER PILING DATE: 1992-10-21
EARLIER PILING DATE: 1992-10-21
EARLIER PILING DATE: 1992-03-11
NUMBER OF SEQ ID NOS: 26
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2424.00
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                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: HUMAN
FRATURE:
NAME/KEY: CDS
LOCATION: (13)..(1389)
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; LOCATION: (124)..(1389)
US-08-260-190-5
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
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US-09-949-016-4332
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Sequence 171, Application US/09949016

Sequence 171, Application US/09949016

SERENTAL INPORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-0-10-03

PRIOR FILING DATE: 2000-0-0-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRELEGG for Windows Version 4.0

SEQ ID NO 1: 20
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US-09-949-016-171
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US-09-949-016-171
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Sequence 23, Application US/08260190A

Patent No. 6774117

GENERAL INFORMATION:

APPLICANT: Zavada, Jan

APPLICANT: Pastorekova, Silvia

APPLICANT: Pastorek, Jaromin

TITLE OF INVERTION: MN Gene and Protein

FILE REFERENCE: D-0021-2

CURRENT APPLICATION: WHOMER: US/08/260,190A

CURRENT FILING DATE: 1994-06-15

EARLIER PILING DATE: 1993-10-30

EARLIER FILING DATE: 1992-10-21

EARLIER PELING DATE: 1992-10-21

EARLIER PILING DATE: 1992-10-21

SARLIER PILING DATE: 1992-10-21

SARLIER PILING DATE: 1992-10-21

SARLIER PILING DATE: 1992-10-21

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PATENTING DATE: 1992-03-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PATENTING DATE: 1992-03-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PATENTING DATE: 1992-03-11
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CLO01307
CURRENT APPLICATION NUMBER: 00/291,016
CURRENT PILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/241,768
FRIOR PILING DATE: 2000-10-20
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NOS: 207012
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Query Match:
DB:
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ORGANISM: Human
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                                                                                                                 MetAlaProLeuCysProSerProTrpLeuProLeuLeuIleProAlaProGly
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                                                     Length:
Matches:
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92.1%
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; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
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US-08-260-190-23
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Query Match:
DB:
                                              Alignment Scores:
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Sequence 1695, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
    APPLICANT: Algate, Paul A.
    APPLICANT: Mannion, Jane
    APPLICANT: Gordon, Brian
    APPLICANT: Harlocker, Susan L.
    APPLICANT: Harlocker, Susan L.
    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
    TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF KIDNEY CANCER
    TITLE OF INVENTION: COMPOSITIONS AND INSTANCES
    TITLE OF INVENTION: COMPOSITIONS AND STRONGS OF KIDNEY CANCER
    TITLE OF INVENTION: 1000511010102,524
    CURRENT FILING DATE: 2002-03-19
    NUMBER OF SEQ ID NOS: 1863
    SEQ ID NO 1695
    SEQ ID NO 1695

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      US-09-954-456-726
US-09-967-706-1080
US-09-968-007A-213
US-10-301-822-11
US-10-465-572-9
US-10-10-25-027-305
US-10-295-027-305
US-10-295-027-1022
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US-10-756-148-295
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Matches:
Conservative:
Mismatches:
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Gaps:
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US-10-921-590-79
US-09-772-719-5
US-09-967-237-5
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US-10-795-933-23
US-10-795-933-1
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Query Match:
DB:
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TYPE: DNA
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 Sequence 1695, Ap
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Sequence 5, Appli
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                                                                   ; Search time 1362 Seconds (without alignments) 2786.817 Million cell updates/sec
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                                                                                                                                1 MAPLCPSPWLPLLIPAPAPG......RRGTKGGVSYRPAEVAETGA 459
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1: /cgn2 6/ptodata1/pubpna/USO1 PUBCOMB.seq:*

2: /cgn2 6/ptodata1/pubpna/USO8 PUBCOMB.seq:*

3: /cgn2 6/ptodata1/pubpna/USO9A PUBCOMB.seq:*

4: /cgn2 6/ptodata1/pubpna/USO9B PUBCOMB.seq:*

5: /cgn2 6/ptodata1/pubpna/USIO8 PUBCOMB.seq:*

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8: /cgn2 6/ptodata1/pubpna/USIOB PUBCOMB.seq:*

9: /cgn2 6/ptodata1/pubpna/USIOB PUBCOMB.seq:*

9: /cgn2 6/ptodata1/pubpna/USIOB PUBCOMB.seq:*

10: /cgn2 6/ptodata1/pubpna/USIOB PUBCOMB.seq:*
          GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                  nucleic search, using frame_plus_p2n model
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US-09-772-119-1
US-09-967-237-1
US-10-723-795-1
US-10-795-933-5
US-10-988-694-1
US-10-921-590-1
                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                   9793542 seqs, 4134689005 residues
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                                                                      February 17, 2006, 15:26:00
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1330 AGGGGAACCAAAGGGGGGTGTGAGCTACCGCCCAGCAGAGGTAGCCGAGACTGGAGCC 1386
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09772719
Patent No. US20020137910A1
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street
STREET: California
COUNTRY: USA
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APPLICATION NUMBER: US/09/772,719
FILING DATE: 30-JAN-2001
CLASSIPICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-UN-1994
ATTORNEY/AGENT INFORMATION:
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TELECOMPUNICATION INFORMATION:
TELEPHONE: 415-981-0334
TELERAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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US-10-723-795-1

Sequence 1, Application US/10723795

Publication No. US20040146955A1

GENERAL INFORMATION:

APPLICANT: Supram, Claudiu

APPLICANT: Supram, Claudiu

APPLICANT: Pastorekova, Silvia

TITLE OF INVENTION: CA IX-SPECIFIC INHIBITORS

FILE REFERENCE: MST-2393 US

CURRENT APPLICATION NUMBER: US/10/723,795

CURRENT APPLICATION NUMBER: 60/429,089

PRIOR FILING DATE: 2003-11-26

PRIOR APPLICATION NUMBER: 60/429,089

PRIOR PILING DATE: 2003-07-22

PRIOR PILING DATE: 2003-07-22

PRIOR PILING DATE: 2003-07-22

PRIOR PILING DATE: 2003-07-22

PRIOR PILING DATE: 2003-07-28

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn Version 3.2

FENDING OF SEQ ID NOS: 9

SOFTWARE: PatentIn Version 3.2
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                                                                                                             TrpArgTyrGlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160
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                                                                GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100
                   ATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGACTCCTCT
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                                                                                       GAACTCCTGGGCTTCCAGCTCCCGCGCGCTCCCAGAACTGCGCCTGCGGCAACAATGGCCAC 612
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Publication No. US20040259126A1
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TILE OF INVENTION: MN Gene and Protein
FILE REFERENCE: D-0021-2
CURRENT APPLICATION NUMBER: US/08/260,190
PRIOR APPLICATION NUMBER: US/08/260,190
PRIOR FILING DATE: 1994-06-15
PRIOR PILING DATE: 1993-12-30
PRIOR PILING DATE: 1992-10-21
PRIOR PILING DATE: 1992-10-21
PRIOR PILING DATE: 1992-10-21
PRIOR PILING DATE: 1992-03-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5 Length: 1.31e-227 2424.00 100.0% 100.0% ORGANISM: HUMAN FRATURE: NAME/KEY: CDS LOCATION: (13)..(1389) FRATURE: ; NAME/KEY: mat_peptide ; LOCATION: (124)..(1389) US-10-795-933-5 Percent Similarity: Best Local Similarity: Query Match: DB: ò

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RESULT 5 US-10-795-933-5

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GInSerproValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu
                                                                                                         SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr
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                                                    GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnAsnGlyHis
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APPLICATION NUMBER: US/10/888,694
FILING DATE: 08-Jul-2004
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION ADATA:
APPLICATION NUMBER: US/09/772,719
FILING DATE: 30-Jan-2001
APPLICATION NUMBER: US 08/485,049
FILING DATE: 30-Jan-1995
ATTORNEY/AGENT: INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REGISTRATION NUMBER: 30,863
REGISTRATION NUMBER: 30,863
REGISTRATION NUMBER: 30,863
REGISTRATION NUMBER: 415-81-2034
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMATION:
TELEFONE: 415-981-332
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
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Matches:
Conservative:
Mismatches:
Indels:
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                                                        ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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2424.00
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CITY: San Francisco
STATE: California
                                     COUNTRY: USA
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Best Local Similarity:
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Pred. No.:
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Pastorek, Jaromir TITLE OF INVENTION: MN Gene and NUMBER OF SEQUENCES: 86 CORRESPONDENCE ADDRESS: ADDRESSEE: Leona L. Lauder

Pastorekova, Silvia

Sequence 1, Application US/10888694 Publication No. US20050003425A1 GENERAL INFORMATION: APPLICANT: Zavada, Jan

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                                   TGGCGCTATGGAGGCGACCCGCCCTGGCCCCGGGTGTCCCCCAGCCTGCGCGGGGCGCTTC
                                                        GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu
                                                                  CAGTCCCCGGTGGATATCCGCCCCCAGCTCGCCGCCTTCTGCCCGGCCCTGCGCCCCTG
                                                                                                  GAACTCCTGGGCTTCCAGCTCCCGCCGCTCCCAGAACTGCGCCTGCGCAACAATGGCCAC
                                                                                                                                                                   CGGGCTCTGCAGCTGCATCTGCACTGGGGGCTGCAGGTCGTCCGGGCTCGGAGCACACT
                                                                                                                                                                                                   PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCygAlaGlnGlyVal
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                                                                                         GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnAsnGlyHis
                                                                                                                                                          ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThr
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Sequence 1, Application US/10921590 Publication No. US20050031623A1 GENERAL INFORMATION: APPLICANT: Pastorek, Jaromir

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APPLICANT: Carcova Gut, Marta
APPLICANT: Carcova Gut, Marta
APPLICANT: Catovicova, Miriam
APPLICANT: Bastorekova, Silvia
APPLICANT: Catovicova, Miriam
APPLICANT: Cavadova, Silvia
APPLICANT: Cavadova, Suzamna
TITLE OF INVENTION: SCUUBLE FORM OF CARRONIC ANHYDRASE IX (a-CA IX), ASSAYS TO DETECT
TITLE OF INVENTION: SCLUBLE FORM OF CARRONIC ANHYDRASE IX (a-CA IX)
TITLE OF INVENTION: IX-SPECIFIC MONOCLONAL ANTIBODIES TO NON-IMMUNODOMINANT EPITOPES
TITLE OF INVENTION: IX-SPECIFIC MONOCLONAL ANTIBODIES TO NON-IMMUNODOMINANT EPITOPES
TITLE OF INVENTION WUMBER: 60/358,824
PRIOR APPLICATION NUMBER: 60/388,08
PRIOR PILING DATE: 2002-05-23
PRIOR PILING DATE: 2002-12-05
PRIOR PILING DATE: 2003-12-05
PRIOR PILING DATE: 2003-02-11
PRIOR PILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: PCT/US03/05136
PRIOR PILING DATE: 2003-02-21
PRIOR FILING DATE: 2003-02-21
PRIOR PILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: PCT/US03/05136
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: PCT/US03/05136
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: PCT/US03/05136
PRIOR PLING DATE: 2003-02-21
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PRIOR PLING DATE: 2003-02-21
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (13)..(1389)
FEATURE:
NAME/KEY: mat peptide
LOCATION: (124)..(1389)
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Best Local Similarity:
Query Match:
DB:
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           CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-22
PRIOR PELING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR PILING DATE: 2000-09-25
PRIOR PILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR PILING DATE: 2000-09-27
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Sequence 89, Application US/09954456

Patent No. US20020115057A1

PATENT NO. US20020115057A1

GENERAL INFORMATION:

APPLICANT: Young, Paul

TITLE OF INVENTION: Seets

TITLE OF INVENTION: Seets

FILE REFERENCE: 689290-76
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       PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR PILING DATE: 2000-09-25
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Fatent No. US20020115057A1
GENERAL INFORMATION:
FATEL INFORMATION:
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
FRIOR FILING DATE: 2000-09-18
FRIOR FILING DATE: 2000-09-18
FRIOR PAPLICATION NUMBER: US/60/234,052
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 X66839
US-09-960-706-1080
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Sequence 1080, Application US/09960706
Publication No. US20030134280A1
GENERAL INFORMATION:
APPLICANT: Munger, William E.
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplas
TITLE OF INVENTION: Gane Expression Profiles
FILE REFERENCE: 44221-5029-01US
CURRENT APPLICATION NUMBER: US/09/960,706
CURRENT APPLICATION NUMBER: 00/223,323
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 1124
SEQ ID NO 1080
LENGTH: 1552
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sequence 516, Application US/09873367C

publication No. US20030165839A1

GENERAL INFORMATION:

APPLICANT: Young, Paul

APPLICANT: Young, Paul

APPLICANT: Reinhard

APPLICANT: Endress, Gregory

APPLICANT: Reinhard

APPLICANT: Reinhard

APPLICANT: Reinhard

APPLICANT: Reinhard

APPLICANT: Carter, Kenneth

TITLE OF INVENTION: Signature Gene Sets

TITLE OF INVENTION: Signature Gene Sets

TITLE OF INVENTION: Signature Gene Sets

FILE REFERENCE: 689290-64

CURRENT APPLICATION NUMBER: U.S. 60/236,891

PRIOR PILING DATE: 2000-09-29

PRIOR PLING DATE: 2000-09-29

PRIOR PLING DATE: 2000-09-29

PRIOR PLING DATE: 2000-11-01

SPOTWARE: Patentin version 3.0

SEQ ID NO 516

LENGTH: 1552
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ORGANISM: Homo
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	401 AlaGlubroValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLe	AlaGluThrG]	; Sequence 119, Application 05/05/05/06/07 ; Publication No. US20040115625A1 ; GENERAL INFORMATION: ; APPLICANT: Ebner, Reinhard ; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Scr ; TITLE OF INVENTION: Gene Sets ; FILE REFERENCE: 689290-71 ; CURRENT APPLICATION NUMBER: US/09/968,007A	COURTENT FILLING DATE: 2001-10-02 PRIOR PRICTON NUMBER: US/60/237,172 PRIOR FILLING DATE: 2000-10-02 PRIOR PELICATION NUMBER: US/60/237,173 PRIOR PELING DATE: 2000-10-02 PRIOR APPLICATION NUMBER: US/60/237,278 PRIOR PILING DATE: 2000-10-02 PRIOR PILING DATE: 2000-10-02 PRIOR PILING DATE: 2000-10-02	PRIOR APPLICATION NUMBER: US/60/237,295 PRIOR FILING DATE: 2000-10-02 PRIOR APPLICATION NUMBER: US/60/237,316 PRIOR FILING DATE: 2000-10-02 NUMBER OF SEQ ID NOS: 1001 SOFTWARE: Patentin version 3.0 SEQ ID NO 213 LENGTH: 1552	TYPE: DNA ORCANISM: Homo sapiens 9-968-007A-213 mment Scores:	Pred. No.: 1.346-227 Length: 1552 Score: 444.00 Matches: 459 Percent Similarity: 100.0\$ Conservative: 0 Best Local Similarity: 100.0\$ Mismatches: 0 Query Match: 3 Gaps: 0 Gaps: 100.0\$ Indels: 0 Gaps: 100.0\$ Gaps: 0	eucysProserProfice 1.1317

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Sequence 11, Application US/10301822

Publication No. US20030148410A1

GENERAL INPORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Guillemette, Tracy L.

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

APPLICANT: Mondan, John E.

APPLICANT: METHODE FOR IDENTIFICATIONS, KITS, AND

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT,

TITLE OF INVENTION: THERAPY OF COLON CANCER

FILE REFERENCE: MPMO1-02922RNM

CURRENT APPLICATION NUMBER: US 60/339, 971

PRIOR PILING DATE: 2002-11-21

PRIOR PELING DATE: 2002-12-05

PRIOR FILING DATE: 2002-03-05

PRIOR FILING DATE: 2002-03-05

PRIOR FILING DATE: 2002-03-05

PRIOR PILING DATE: 2002-03-05

PRIOR PELING DATE: 2002-03-05

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PRIOR PILING DATE: 2000-03-05

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GAACTCCTGGGCTTCCAGCTCCCGCCGCTCCCAGAACTGCGCCTGCGCAACAATGGCCAC
                                                        ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThr
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APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
PRIOR PILICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
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Publication No. US20030224374A1
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Hinsley, Peter
APPLICANT: Mao, Mao
APPLICANT: Roberts, Chris
APPLICANT: Van t' Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
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Matches:
Conservative:
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Indels:
                                                      Sequence 9, Application US/10465572
Sequence 9, Application US/10465572
Publication No. US20030207840A1
GENERAL INFORMATION:
APPLICANT: Riggins Gregory
ITTLE OF INVENTION: GENES INDUCED BY HYPOXIA
FILE REFERENCE: 000250.00012
CURRENT APPLICATION NUMBER: US/10/465,572
CURRENT FILING DATE: 2003-06-20
FRIOR PRICH FLING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/307,600
FRIOR FILING DATE: 2001-07-26
NUMBER OF SEQ ID NOS: 30
SOFTWARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
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ORGANISM: Homo sapiens
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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; SEQ ID NO 574
; SEQ ID NO 574
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_001216
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-574
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
Score:
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Sequence:

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Sequence 19, Application US/11112944

Publication No. US20050244872A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Breast Cancer Gene Expression Biomarkers

FILE REFERENCE: 05-325-US

CURRENT FILING DATE: 2005-04-22

PRIOR APPLICATION NUMBER: US/11/112,944

CURRENT FILING DATE: 2004-04-23

PRIOR FILING DATE: 2004-04-23

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin version 3.3

LENGTH: 1552
                US-11-072-175-87

US-11-0056-88-633

US-10-055-877-15

US-10-055-877-15

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US-11-136-527-5212

US-11-136-527-5212

US-11-136-527-5459

US-11-136-527-2459

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US-11-112-944-19
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      -MODEL-frame+ pan.model - DEV=xlp
-QA/abss/ABSSWEB spool/US0967237/runat_15022006_182256_28276/app_query.fasta_1
-QA/abss/ABSSWEB spool/US09967237/runat_15022006_182256_28276/app_query.fasta_1
-QA-Abss/ABSSWEB spool/US09967237/runat_pasta_n_SUPFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 - SND=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-MAXIEN=2000000000 -HOST=abss06p
-USER=US09967237 @CGN 1 1 335 @runat_15022006_182256_28276_-NCPU=6 -ICPU=3
-USER=US09967237 @CGNS=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
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Sequence 11, Appl
Sequence 73, Appl
Sequence 73, Appl
                                                                                                                                       ; Search time 518 Seconds (without alignments)
1880.959 Million cell updates/sec
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1 MAPLCPSPWLPLLIPAPAPG......RRGTKGGVSYRPAEVAETGA 459
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1. /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

2. /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

3. /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

4. /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

5. /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

6. /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

7. /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

8. /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

9. /cgn2_6/ptodata/1/pubpna/USI0_NEW_PUB.seq:*

10. /cgn2_6/ptodata/1/pubpna/USI1_NEW_PUB.seq:*

11. /cgn2_6/ptodata/1/pubpna/USI1_NEW_PUB.seq:*

12. /cgn2_6/ptodata/1/pubpna/USI1_NEW_PUB.seq:*

13. /cgn2_6/ptodata/1/pubpna/USI1_NEW_PUB.seq:*

13. /cgn2_6/ptodata/1/pubpna/USI1_NEW_PUB.seq:*
                      GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                   nucleic search, using frame plus p2n model
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2 US-11-186-284-11
US-10-063-703-73
2 US-11-102-240-73
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Minimum DB Maximum DB

Sequence 62901, A Sequence 62901, A Sequence 62901, A Sequence 932, App Sequence 236, App Sequence 1683, App Sequence 1683, App Sequence 5779, App Sequence 5779, App Sequence 5779, App Sequence 3, App Sequence 5, App Sequence 6, App Seque

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GREREAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Gaillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Haracy L.
APPLICANT: Haracy L.
APPLICANT: Haracy L.
APPLICANT: Monahan, John E.
APPLICANT: Haracy L.
APPLICANT: Monahan, John E.
APPLICANT: APPLICATION NUMBER: US/10/301,822
FRIOR PILING DATE: 2002-10-10
FRIOR FILING DATE: 2002-11-10
FRIOR FILING DATE: 2002-11-10
FRIOR FILING DATE: 2002-03-05
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ORGANISM: Homo Sapiens
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Best Local Similarity:
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; LOCATION: (43)
US-11-186-284-11
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US-09-967-237B-2 (1-459) x US-11-112-944-19 (1-1552)
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APPLICANT: Godward, Paul J.
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APPLICANT: Grimaldi, Christopher J.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,703
CURRENT APPLICATION NUMBER: 2002-05-08
Prior Application removed - See Palm or File Wrapper
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                                                                                                                                                                                                                                                     Sequence 73, Application US/10063703; Publication No. US/20060008901A1; GENERAL INFORMATION: APPLICANT: Baton, Dan L. APPLICANT: Filvaroff, Ellen
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US-10-063-703-73
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LOCATION: 1528
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351 ACATGGTCAGGACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCC 410
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                                                           291 GCTGGAGGTGATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCC 350
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                                                                                    -GlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPheGlnSerPr
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APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESSI;
TITLE OF INVENTION: ASSPHAGAL TUMOR
FILE OF INVENTION: ASSPHAGAL TUMOR
FILE REFERENCE: P3230RIC106C
CURRENT APPLICATION NUMBER: US/11/102,240
CURRENT APPLICATION NUMBER: 10/003662
PRIOR PRILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-12-06
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 199-12-09
INDMER OF SEQ ID NOS: 170
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|231 CCTCAAATTCCCAGTCCCCTGCACCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCT
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Matches:
Conservative:
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Sequence 73, Application US/11102240
Publication No. US20050260647A1
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown base
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ORGANISM: Homo Sapien
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OTHER INFORMATION:
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Best Local Similarity:
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NAME/KEY: unsure
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PRIOR FILING DATE: 2001-08-02
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                                                                                                                                                                                                                                                      eSerArgTyrPheClnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVall1 341
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                                                                  uGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgPro---GlySerGluHisThrValGl 242
                                                                                                                 CCAGCTCCACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGTCAGAACACCAGATCAA 647
                                                                                                                                                            CAGTGAAGCCACATTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAG 707
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                                                                                                                                              242 uGlyHisArgPheProAlaGluIleHisValValHisLeu---SerThrAlaPheAlaAr 261
                                                                                                                                                                                                                 CTTGAGTGAGGCTGAGAGGCCTCAGGCCTGGCTGTCCTGGGCATCCTAATTGAGGT 767
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                                                                                                                                                                                                                                                                                     uGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAspPh 321
                       nLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyrArgAlaLe
           uGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnAsnGlyHisSerValGl
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Publication No. US20050260572A1

GENERAL INFORMATION:

APPLICANT: DNA Chip Reasearch Inc.

APPLICANT: Hitachi Software Engineering Co., Ltd.

TITLE OF INVENTION: A method of predicting cancer condition

FILE REFERENCE: PH-1533-PCT

CURRENT APPLICATION NUMBER: US/10/276,233A

CURRENT APPLICATION NUMBER: US/10/276,233A

FRIOR FILING DATE: 2001-13063

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-04-06

PRIOR FILING DATE: 2001-04-06

PRIOR PLING DATE: 2001-04-06
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LeuArgLeuArgAsnAsnGlyHisSerValGlnLeuThrLeuProProGlyLeuGluMet 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheCysProAlaLeuArgProLeuGluLeuLeuGlyPheGlnLeuProProLeuProGlu 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 TTTCTCCTGACCAACAATGGCCATTCAGTGAAGCTGAACCTGCCCTCGGACATGCAACAT 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 AlaLeuGlyProGlyArgGluTyrArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAla 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           491 AATGACCGCACGCACGCTCTGAGCACACCGTCAGCGGACAGCACTTCGCCGCAGCTGCACCTCGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 GlyArgPro---GlySerGluHisThrValGluGlyHisArgPheProAlaGluIleHis 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValValHisLeu---SerThrAlaPheAlaArgValAspGluAlaLeuGlyArgProGly 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          551 ATTGFCCAFTATAACTCAGACCTTTATCCTGACGCCAGCACTGCCAGCAACAAGTCAGAA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TICAACATIGAAGACTGCTTCCGGAGAGGACGCTGAATATTACCGCTACCGGGGGTCC 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 CACGCGGCGGCCGTGCTCCTGGTGATCTTAAAGGAACAGCCTTCCAGCCCCGGCCCCA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 GTGAACGGTTCCAAGTGGACTTATTTTGGTCCTGATGGGGAGAATAGCTGGTCCAAGAAG
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Matches:
Conservative:
Mismatches:
Indels:
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LOCATION: (2658), (2660), (2753)
OTHER INFORMATION: n is a, c, 9
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542.50
47.2%
35.2%
22.4%
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 21
LENGTH: 2771
                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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The Cartifaction of

193 GTGAACGGTTCCAAGTGGACTTATTTTGGTCCTCAAGGGGAGAATAGTGTGCTCCAAGAAG 153 SePPLOAL ALGUALGGAGGCCTGCTGCACGCACAGGGGGAGAATAGTGACTCCTCAAGAAG 173 PheCysProAlaLeuArgPheGIDseProValAgaII laxgProGIDLeuArgLogUu 19 174 TATCACGCCGGCTCCCCCCCATCAGGCTCCACCCATCACCTCCACAGCAGG 37 175 LeuArgleuArgAsnAsnOlyHisSerValGIDLeuThrLeuProProGlyLeuGluMet 21 176 TATCCTCCTACCACACACTCCCCCCCATCAGGCTCCACACTCGCCCCCCCC	Qy 406 LeudsbiserCysLeudlaAlaGlyAspileLeudlaIbedValPheGlyLeuLeuPheAla 425 Db 989 GTGCAAGTCTGCGGGACTGAGTCTGGGGGATCATCCTCTCATGGCCTGGCT 1048 Qy 426
788 CTGACCACCCCCTTGCAACCCCCATGGGCACACGGGCACGGGGGGGG	Pred. No.: 3.01e-27

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347 GlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSerAspThrLeuTrp---Gly 365
327 TyrGluGlySerLeuThrThrProProCysAlaGlnGlyVallleTrpThrValPheAsn 346
                                                                                                                                                                                                                                 366 ProGlyAspSerArgLeuGlnLeu----AsnPheArgAlaThrGlnProLeuAsnGly 383
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TITLE OF INVENTION: Novel Polypeptides and Mucleic Acids Encoded Thereby
TITLE OF INVENTION: Novel Polypeptides and Mucleic Acids Encoded Thereby
CURLENT APPLICATION NUMBER: US/10/055,877
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262,892
                                                                                           766 CGCGTGGTAAAGGCCTCCTTCCGGGCC 792
                                                                                                                                                                                                                                                                                                                   384 ArgvalileGluAlaSerPheProAla 392
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PRIOR APPLICATION NUMBER: 60/263,598
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,799
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264,117
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PRIOR APPLICATION NUMBER: 60/264,139
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263,351
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APPLICATION NUMBER: 60/263,351
FILING DATE: 2001-01-30
APPLICATION NUMBER: 60/272,870
FILING DATE: 2001-03-02
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APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Tohernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Ballinger, Robert
APPLICANT: Sprek, Kimberly
APPLICANT: Ratelli, Luca
APPLICANT: Ratelli, Luca
APPLICANT: Rekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/10055877 Publication No. US20050288241A1 GENERAL INFORMATION:
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Taupier Jr., Raymond
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Shimkets, Richard
Gusev, Vladimir
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Burgess, Cahterine
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Zerhusen, Bryan
Andrew, David
Mezes, Peter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eisen, Andrew
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                                                              APPLICANT: BERTUCZI, Francois
APPLICANT: BERTUCZI, Remi
APPLICANT: BIRNBAUM, Daniel
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
PILE REPERENCE: 1423-R-03
CURRENT APPLICATION NUMBER: US/11/000,688
CURRENT FILING DATE: 2004-12-01
PRIOR PILING DATE: 2003-12-01
NUMBER OF SEQ ID NOS: 1596
SOFTWARE: Patentin version 3.2
SEQ ID NO 633
LENGTH: 1428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287 SerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAlaGluGluGlySerGluThr 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LeuGluMetAlaLeuGlyProGlyArgGluTyrArgAlaLeuGlnLeuHisLeu 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 GlnValProGlyLeuAspIleSerAlaLeuLeuProSerAspPheSerArgTyrPheGln 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgProLeuGluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsn 197
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OTHER INFORMATION: Description of Artificial sequences:primer
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101
41
99
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COTHER INFORMATION: carbonic anhydrase vii(CA7) gene US-11-000-688-633
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Matches:
Conservative:
Mismatches:
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      Sequence 633, Application US/11000688 Publication No. US20050287544A1 GENERAL INFORMATION:
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409.00
52.8%
37.5%
16.9%
                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity:
Query Match:
DB:
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Service Assessment

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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 828
TYPE: DNA
                                                                                                         379 nProLeuAsnGlyArgVallleGluAlaSerPhe 390
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PRIOR FILING DATE: 2001-01-23
PRIOR PLING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2001-01-25
PRIOR PELING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR PILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR APPLICATION NUMBER: 60/20,970
PRIOR PILING DATE: 2001-03-02
PRIOR PILING DATE: 2001-03-04
PRIOR PILING DATE: 2001-03-04
PRIOR PILING DATE: 2001-03-07
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-14
                                                                                                                                                                                                      Sequence 15, Application US/10055877
Sequence 15, Application US/10055877
Publication No. US20050288241A1
GENERAL INFORMATION:
APPLICANT: Dedigaru, Muralidhara
APPLICANT: Padigaru, Muralidhara
APPLICANT: Tchernev, Velizar
APPLICANT: Tchernev, Velizar
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Spytek, Kimberly
APPLICANT: Spytek, Kimberly
APPLICANT: Ratelli, Luca
APPLICANT: Ratelli, David
APPLICANT: Rannesh
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APPLICANT: Andrew, David
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Shimkets, Richard
Gusev, Vladimir
Vernet, Corine
Taupier Jr., Raymond
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Burgess, Cahterine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 GCAGGTTCACCTTCACTGGGGGTCCGCTGATGACCACGGCTCCGAGCACATAGTAGATGG 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 uProProLeuProGluLeuArgLeuArgAsnAsnGlyHisSerValGlnLeuThrLeuPr 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 oProGlyLeuGluMetAlaLeu-----GlyPro---GlyArgGluTyrArgAlaLe
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 333
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98
41
116
17
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Mismatches:
Indels:
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Matches:
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378.00
51.18
36.0%
15.6%
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US-10-055-877-17
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uSerAspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGl 379
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APPLICANT: Caeman, Stacie
APPLICANT: Caeman, Stacie
APPLICANT: Caeman, Stacie
APPLICANT: Caeman, Stacie
APPLICANT: Boldog, Ference
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR FILING DATE: 2001-01-19
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527 AAGACTGAGGACAĆATGTTAAGGGGGCAGAAĆTÝGTCGAAGGCTGTGAĆGGGATTTŤTGGG 568
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                                                APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE ON INVENTION: Probe Arrays For Expression Profiling
FILE REPERRNCE: 031896-041000 (AM101086)
CURRENT PEPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-06-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-06-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1116
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Matches:
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        Sequence 1116, Application US/11136527 Publication No. US20050287570A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         1.96e-15
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Best Local Similarity:
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Indels:
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 ; OKGANISM: Homo sapien;
; PEATURE:
; NAME/KEY: CDS
; LOCATION: (16)..(801)
US-10-055-877-15
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                                                     261 gValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGluGl
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                                                                                                                    281 uGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIJeAlaGl
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; Publication No. US20060029956A1
; GENERAL INFORMATION:
; APPLICANT: Beyer, Wayne F.
; APPLICANT: Beyer, Wayne F.
; APPLICANT: Beyer, Wayne F.
; APPLICANT: Greelke, John W.
; APPLICANT: Blaesius, Rainer H.
; TITLE OF INVENTION: DETECTION OF OVARIAN DISEASE
; TITLE OF INVENTION: DETECTION OF OVARIAN DISEASE
; TILE REFERENCE: 46143/294851
; CURRENT FPLING DATE: 2005-07-08
; PRIOR FLILING DATE: 2005-07-09
; PRIOR FLILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FaetSEQ for Windows Version 4.0
; SEQ ID NO 5
; LEMETHER FOR THE FAETSEQ FOR WINDOWS VERSION 4.0
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ORGANISM: Homo sapiens
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APPLICANT: Woute, William M
APPLICANT: Wounte, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294
NUMBER OF SEQ ID NOS: 362810
SOFTWARE: PatentIn version 3.2
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US-11-136-527-5212
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APPLICANT: BERTUCCI, Francois
APPLICANT: HOULGATTE, Remi
APPLICANT: BIRNBAUM, Daniel
APPLICANT: BIRNBAUM, Daniel
APPLICANT: BIRNBAUM, Daniel
APPLICANT: BIRNBAUM, Daniel
APPLICANTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
FILE REPERBNCE: 1423-R-03
CURRENT APPLICATION NUMBER: US/11/000,688
CURRENT FILING DATE: 2004-12-01
PRIOR APPLICATION NUMBER: US 60/525,987
PRIOR FILING DATE: 2003-12-01
NUMBER OF SEQ. DATE: 1596
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Sequence 845, Application US/11000688 Publication No. US20050287544A1 GENERAL INFORMATION:
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APPLICANT: Woth
APPLICANT: Wounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat (
FILE REFERENCE: 031896-041000 (AMIO1086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT PILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-06-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 3817
LENGTH: 1201
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              Sequence 3817, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
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                                CAACGGTCCTGACCACTGGCATGAACTTTTCCCAAATGCCAAGGGGGAAAACCAGTCGCC 772
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                                                                 OValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeuGluLeuLe 183
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-GlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPheGlnSerPr
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                      101 LysSerGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaPro--- 119
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TrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSerAsp 361
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wounts, William M
APPLICANT: Wounts, William M
APPLICANT: Wounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes FILE REFERENCE: 031896-041000 (AMIOLO86)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR PILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SEQ ID NO 556
LENGTH: 1858
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; Sequence 556, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
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US-11-136-527-556
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CATGGCTCTGAGCACACAGTGGAGTGGAGTGAGTATGCTGCTGAGCTTCACCTGGTTCAC
                                                                                                             274 lLeuAlaAlaPheLeuGluGluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSe
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                                                 LeuSerThrAlaPhe-AlaArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaVa
                                                                              regaaccceaagraraacaccrrcegaegaegcrcrcaaagcaegcccearegearrecrer
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